

SEQUENCE LISTING

<110> Vreeland, Valerie
 The Regents of the University of California

<120> Recombinant Minimal Catalytic Vanadium Haloperoxidases
 and Their Uses

<130> 023070-087110US

<140> US 09/596,794
 <141> 2000-06-19

<150> US 09/151,189
 <151> 1998-09-10

<160> 20

<170> PatentIn Ver. 2.1

<210> 1
 <211> 2931
 <212> DNA
 <213> Fucus distichus

<220>
 <221> CDS
 <222> (228)..(2258)
 <223> vanadium bromoperoxidase

<400> 1
 cgcggacaag ctttggaga gaggttgc aattcaacag agcgaggccc gtgaagggtgt 60
 ggaggacacg tgctacaaggc tgatccacga gagcctcaac ttccctactg atacgggagt 120
 ttgtactgcg ccgcgttgcc aaaaaccgca actttaaaca gcgcctcgca ggcacatg 180
 cttcccacgc atccacaaaa tcgacagtgg tattcgctgag cttgaat atg ctt tgc 236
 Met Leu Cys
 1

cat gca gcg qac acg aca aga ggc tct cct atg cct gac acc gga gtg 284
 His Ala Ala Asp Thr Arg Gly Ser Pro Met Pro Asp Thr Gly Val
 5 10 15

ctt cgg ttg ctc aca tca gag cag cgc gct aaa ggt tgg aga cgc cag 332
 Leu Arg Leu Leu Thr Ser Glu Gln Arg Ala Lys Gly Trp Arg Arg Gln
 20 25 30 35

tta gag ggg gag aaa tca cta ggt ttt cat cca agc gag acg cct tat 380
 Leu Glu Gly Glu Lys Ser Leu Gly Phe His Pro Ser Glu Thr Pro Tyr
 40 45 50

atc aag tac ttg gaa ggc tct gag act tgg aag aag gtt aag ctt cca 428
 Ile Lys Tyr Leu Glu Gly Ser Glu Thr Trp Lys Lys Val Lys Leu Pro
 55 60 65

acg gac ggc ata tcg gct tcc aag atc ctg ggt aaa att atg gcc agg 476
 Thr Asp Gly Ile Ser Ala Ser Lys Ile Leu Gly Lys Ile Met Ala Arg
 70 75 80

gtc cgc atc gct acc gcc ttg gct gtg gta ctg gcc gca ccc tgt ttg	524
Val Arg Ile Ala Thr Ala Leu Ala Val Val Leu Ala Ala Pro Cys Leu	
85 90 95	
gca ttc gac gag gtc aca gcc agt ggt gtt ttc cct gag gaa cac aag	572
Ala Phe Asp Glu Val Thr Ala Ser Gly Val Phe Pro Glu Glu His Lys	
100 105 110 115	
cac acc ggg gag gga aga cac ctc cag acc tgt aca aac tcc gac gat	620
His Thr Gly Glu Gly Arg His Leu Gln Thr Cys Thr Asn Ser Asp Asp	
120 125 130	
gcg ctg gat ccg acg gcg ccg aat aga agg gac aac gta gct ttt gcg	668
Ala Leu Asp Pro Thr Ala Pro Asn Arg Arg Asp Asn Val Ala Phe Ala	
135 140 145	
tcg cgg cgc gat gcc gcc agg cga gaa cgt gac ggg aca ggg act gtc	716
Ser Arg Arg Asp Ala Ala Arg Arg Glu Arg Asp Gly Thr Gly Thr Val	
150 155 160	
tgc caa atc act aac gga gaa act gat ttg gct acc atg ttc cac aag	764
Cys Gln Ile Thr Asn Gly Glu Thr Asp Leu Ala Thr Met Phe His Lys	
165 170 175	
tct ctg cca cac gat gaa ctg gga cag gta acc gca gac gac ttc gct	812
Ser Leu Pro His Asp Glu Leu Gly Gln Val Thr Ala Asp Asp Phe Ala	
180 185 190 195	
atc ctc gag gac tgc atc tta aac gga gat ttc agc att tgc gag gac	860
Ile Leu Glu Asp Cys Ile Leu Asn Gly Asp Phe Ser Ile Cys Glu Asp	
200 205 210	
gtg cct gcg gga gac ccg gcg ggt cgc ctc gtc aat cct acc gct gcg	908
Val Pro Ala Gly Asp Pro Ala Gly Arg Leu Val Asn Pro Thr Ala Ala	
215 220 225	
ttt gcc atc gac ata tcc ggt ccc gca ttc tcg gct acg aca ata ccc	956
Phe Ala Ile Asp Ile Ser Gly Pro Ala Phe Ser Ala Thr Thr Ile Pro	
230 235 240	
ccg gta cct acc ctt tcc tct cct gag ctc gcc gct cag ttg gcg gag	1004
Pro Val Pro Thr Leu Ser Ser Pro Glu Leu Ala Ala Gln Leu Ala Glu	
245 250 255	
cta tac tgg atg gcg ctg gcc agg gat gta ccc ttt atg cag tat ggc	1052
Leu Tyr Trp Met Ala Leu Ala Arg Asp Val Pro Phe Met Gln Tyr Gly	
260 265 270 275	
acc gac gaa att acc act acc gcg gca gcc aac ctc gct gga atg gga	1100
Thr Asp Glu Ile Thr Thr Ala Ala Ala Asn Leu Ala Gly Met Gly	
280 285 290	
ggc ttc cca aat ctg gac gcc gtg tcg ata ggg tcc gat ggt acg gtg	1148
Gly Phe Pro Asn Leu Asp Ala Val Ser Ile Gly Ser Asp Gly Thr Val	
295 300 305	
gac ccg ttc tcc cag ctc ttc cga gcg acc ttc gtt ggt gtt gaa acg	1196
Asp Pro Phe Ser Gln Leu Phe Arg Ala Thr Phe Val Gly Val Glu Thr	
310 315 320	

ggg ccc ttt gtc tct cag ctg ctc gtg aac agc ttc acc atc gac gct	1244
Gly Pro Phe Val Ser Gln Leu Leu Val Asn Ser Phe Thr Ile Asp Ala	
325 330 335	
att acg gtc gaa ccg aag cag gag aca ttc gcc ccc gac ttg aac tat	1292
Ile Thr Val Glu Pro Lys Gln Glu Thr Phe Ala Pro Asp Leu Asn Tyr	
340 345 350 355	
atg gtc gat ttt gac gaa tgg ctg aac att cag aat ggt gga ccc ccg	1340
Met Val Asp Phe Asp Glu Trp Leu Asn Ile Gln Asn Gly Gly Pro Pro	
360 365 370	
gcc ggc ccc gaa gag tta gac gaa gag ctg cgt ttt atc cgt aac gcc	1388
Ala Gly Pro Glu Glu Leu Asp Glu Glu Leu Arg Phe Ile Arg Asn Ala	
375 380 385	
cgc gac ctg gcc agg gtc tcc ttc gtg gac aat atc aac acc gaa gct	1436
Arg Asp Leu Ala Arg Val Ser Phe Val Asp Asn Ile Asn Thr Glu Ala	
390 395 400	
tat cgc ggg tct ctt atc cta ctt gag ctg gga gcc ttc agc agg ccc	1484
Tyr Arg Gly Ser Leu Ile Leu Leu Glu Leu Gly Ala Phe Ser Arg Pro	
405 410 415	
ggt atc aac ggt cca ttc atc gac agt gat cgg cag gcg ggc ttc gtc	1532
Gly Ile Asn Gly Pro Phe Ile Asp Ser Asp Arg Gln Ala Gly Phe Val	
420 425 430 435	
aac ttc ggc acg tct cac tac ttc aga ttg ata ggt gcc gcc gag ctg	1580
Asn Phe Gly Thr Ser His Tyr Phe Arg Leu Ile Gly Ala Ala Glu Leu	
440 445 450	
gcg cag cgt gcc tcg tgt tac caa aag tgg cag gtg cat cga ttt gca	1628
Ala Gln Arg Ala Ser Cys Tyr Gln Lys Trp Gln Val His Arg Phe Ala	
455 460 465	
cgc ccc gag gct ctc ggg ggt acc ctc cac aac acc atc gcg ggg gat	1676
Arg Pro Glu Ala Leu Gly Thr Leu His Asn Thr Ile Ala Gly Asp	
470 475 480	
cta gat gca gac ttc gac atc tcc ctt ctt gaa aat gat gag ctc ttg	1724
Leu Asp Ala Asp Phe Asp Ile Ser Leu Leu Glu Asn Asp Glu Leu Leu	
485 490 495	
aaa cgt gtg gcg gag ata aat gcg gcg cag aat ccc aac aac gag gtc	1772
Lys Arg Val Ala Glu Ile Asn Ala Gln Asn Pro Asn Asn Glu Val	
500 505 510 515	
acc tac ctt ctt cca caa gct atc caa gtg gga tcg cca acg cac cct	1820
Thr Tyr Leu Leu Pro Gln Ala Ile Gln Val Gly Ser Pro Thr His Pro	
520 525 530	
tcc tac ccg tcc ggc cac gct acc caa aat gga gca ttt gcc aca gtt	1868
Ser Tyr Pro Ser Gly His Ala Thr Gln Asn Gly Ala Phe Ala Thr Val	
535 540 545	
ctg aag gcc ctc att ggc cta gat cgg gga ggt gag tgc ttc cct aac	1916
Leu Lys Ala Leu Ile Gly Leu Asp Arg Gly Gly Glu Cys Phe Pro Asn	
550 555 560	

ccc gtg ttc cca agc gat gac ggc ctg gaa cta atc aac ttc gaa ggg	1964
Pro Val Phe Pro Ser Asp Asp Gly Leu Glu Leu Ile Asn Phe Glu Gly	
565 570 575	
gca tgc ctt aca tat gag gga gag atc aac aag ctc gcg gtc aac gtc	2012
Ala Cys Leu Thr Tyr Glu Gly Glu Ile Asn Lys Leu Ala Val Asn Val	
580 585 590 595	
gca ttt ggg agg cag atg ctg ggc atc cac tat cgg ttc gac ggt atc	2060
Ala Phe Gly Arg Gln Met Leu Gly Ile His Tyr Arg Phe Asp Gly Ile	
600 605 610	
caa ggc cta ctt ctc gga gag aca atc act gta cga aca ctt cac cag	2108
Gln Gly Leu Leu Leu Gly Glu Thr Ile Thr Val Arg Thr Leu His Gln	
615 620 625	
gag ctg atg acg ttc gcc gag gaa gcc acc ttt gaa ttc cgc tta ttc	2156
Glu Leu Met Thr Phe Ala Glu Ala Thr Phe Glu Phe Arg Leu Phe	
630 635 640	
acc gga gag gtc atc aaa ctt ttc cag gac ggg aca ttc tcc atc gat	2204
Thr Gly Glu Val Ile Lys Leu Phe Gln Asp Gly Thr Phe Ser Ile Asp	
645 650 655	
gga gat atg tgt tcc ggt ttg gtt tac act ggc gtg gcg gac tgc cag	2252
Gly Asp Met Cys Ser Gly Leu Val Tyr Thr Gly Val Ala Asp Cys Gln	
660 665 670 675	
gct tagtgcagaa aataataatt gtcggatgct taaaatgcac ccacgaccaa	2305
Ala	
gtcgtcgagt cacgtcgccg gagcatcctt cagcgaaaaa ggagagtaac ctatatgcta	2365
tagaggagaa ccacggagta caatgcaggt tctttacca tgtacattgg attgcagtaa	2425
gtgcggtagt agagggatac gttaaacgtg cttgcctgtg tatatgatac atttgcgtat	2485
gaaatattag aatgcgttga cttgacttca ccatgaaata ccatgatcgc gtgggtgtgt	2545
gtttcacct gtcggagcgg tacgtaagat gtgtttcta ctgagccgtt tgtgttttagt	2605
ccattcccgcg tggcagtgtt aacaaagagg atgttgttca gcccctcagtt tggagagtac	2665
cgttaggtggc aggacgtata tctctggtag cggctgttta agaacttcca caagaccgtt	2725
tacgttttgtt tggttagtgc atgccttctc gttacttgac cgatccattt agagtacccgt	2785
taccagtatg gtgtaagaca tattttctc ctgttatgga tctgtagaac agcttaggtgt	2845
tgtttataac acaggatgct ataaaatagg gatgttgata atggcatcgg tactcatgaa	2905
accgcaaaat ggcgatagat attccc	2931

<210> 2
 <211> 676
 <212> PRT
 <213> *Fucus distichus*

<400> 2
 Met Leu Cys His Ala Ala Asp Thr Thr Arg Gly Ser Pro Met Pro Asp
 1 5 10 15
 Thr Gly Val Leu Arg Leu Leu Thr Ser Glu Gln Arg Ala Lys Gly Trp
 20 25 30
 Arg Arg Gln Leu Glu Gly Glu Lys Ser Leu Gly Phe His Pro Ser Glu
 35 40 45
 Thr Pro Tyr Ile Lys Tyr Leu Glu Gly Ser Glu Thr Trp Lys Lys Val
 50 55 60
 Lys Leu Pro Thr Asp Gly Ile Ser Ala Ser Lys Ile Leu Gly Lys Ile
 65 70 75 80
 Met Ala Arg Val Arg Ile Ala Thr Ala Leu Ala Val Val Leu Ala Ala
 85 90 95
 Pro Cys Leu Ala Phe Asp Glu Val Thr Ala Ser Gly Val Phe Pro Glu
 100 105 110
 Glu His Lys His Thr Gly Glu Gly Arg His Leu Gln Thr Cys Thr Asn
 115 120 125
 Ser Asp Asp Ala Leu Asp Pro Thr Ala Pro Asn Arg Arg Asp Asn Val
 130 135 140
 Ala Phe Ala Ser Arg Arg Asp Ala Ala Arg Arg Glu Arg Asp Gly Thr
 145 150 155 160
 Gly Thr Val Cys Gln Ile Thr Asn Gly Glu Thr Asp Leu Ala Thr Met
 165 170 175
 Phe His Lys Ser Leu Pro His Asp Glu Leu Gly Gln Val Thr Ala Asp
 180 185 190
 Asp Phe Ala Ile Leu Glu Asp Cys Ile Leu Asn Gly Asp Phe Ser Ile
 195 200 205
 Cys Glu Asp Val Pro Ala Gly Asp Pro Ala Gly Arg Leu Val Asn Pro
 210 215 220
 Thr Ala Ala Phe Ala Ile Asp Ile Ser Gly Pro Ala Phe Ser Ala Thr
 225 230 235 240
 Thr Ile Pro Pro Val Pro Thr Leu Ser Ser Pro Glu Leu Ala Ala Gln
 245 250 255
 Leu Ala Glu Leu Tyr Trp Met Ala Leu Ala Arg Asp Val Pro Phe Met
 260 265 270
 Gln Tyr Gly Thr Asp Glu Ile Thr Thr Ala Ala Ala Asn Leu Ala
 275 280 285
 Gly Met Gly Gly Phe Pro Asn Leu Asp Ala Val Ser Ile Gly Ser Asp
 290 295 300
 Gly Thr Val Asp Pro Phe Ser Gln Leu Phe Arg Ala Thr Phe Val Gly
 305 310 315 320

Val Glu Thr Gly Pro Phe Val Ser Gln Leu Leu Val Asn Ser Phe Thr
 325 330 335
 Ile Asp Ala Ile Thr Val Glu Pro Lys Gln Glu Thr Phe Ala Pro Asp
 340 345 350
 Leu Asn Tyr Met Val Asp Phe Asp Glu Trp Leu Asn Ile Gln Asn Gly
 355 360 365
 Gly Pro Pro Ala Gly Pro Glu Glu Leu Asp Glu Glu Leu Arg Phe Ile
 370 375 380
 Arg Asn Ala Arg Asp Leu Ala Arg Val Ser Phe Val Asp Asn Ile Asn
 385 390 395 400
 Thr Glu Ala Tyr Arg Gly Ser Leu Ile Leu Leu Glu Leu Gly Ala Phe
 405 410 415
 Ser Arg Pro Gly Ile Asn Gly Pro Phe Ile Asp Ser Asp Arg Gln Ala
 420 425 430
 Gly Phe Val Asn Phe Gly Thr Ser His Tyr Phe Arg Leu Ile Gly Ala
 435 440 445
 Ala Glu Leu Ala Gln Arg Ala Ser Cys Tyr Gln Lys Trp Gln Val His
 450 455 460
 Arg Phe Ala Arg Pro Glu Ala Leu Gly Gly Thr Leu His Asn Thr Ile
 465 470 475 480
 Ala Gly Asp Leu Asp Ala Asp Phe Asp Ile Ser Leu Leu Glu Asn Asp
 485 490 495
 Glu Leu Leu Lys Arg Val Ala Glu Ile Asn Ala Ala Gln Asn Pro Asn
 500 505 510
 Asn Glu Val Thr Tyr Leu Leu Pro Gln Ala Ile Gln Val Gly Ser Pro
 515 520 525
 Thr His Pro Ser Tyr Pro Ser Gly His Ala Thr Gln Asn Gly Ala Phe
 530 535 540
 Ala Thr Val Leu Lys Ala Leu Ile Gly Leu Asp Arg Gly Gly Glu Cys
 545 550 555 560
 Phe Pro Asn Pro Val Phe Pro Ser Asp Asp Gly Leu Glu Leu Ile Asn
 565 570 575
 Phe Glu Gly Ala Cys Leu Thr Tyr Glu Gly Glu Ile Asn Lys Leu Ala
 580 585 590
 Val Asn Val Ala Phe Gly Arg Gln Met Leu Gly Ile His Tyr Arg Phe
 595 600 605
 Asp Gly Ile Gln Gly Leu Leu Gly Glu Thr Ile Thr Val Arg Thr
 610 615 620
 Leu His Gln Glu Leu Met Thr Phe Ala Glu Glu Ala Thr Phe Glu Phe
 625 630 635 640

```
<210> 3
<211> 51
<212> DNA
<213> Artificial Sequence
```

<220>
<223> Description of Artificial Sequence:probe for
second conserved region between Curvularia and
Ascophyllum vanadium peroxidase active sites

<400> 3
ccaaacqccacc cttcgtaccc gtctggccac gctacccaaa acggaggcatt t 51

```
<210> 4
<211> 51
<212> DNA
<213> Artificial Sequence
```

<220>
<223> Description of Artificial Sequence:probe for third
conserved region between Curvularia and
Ascophyllum vanadium peroxidase active sites

<400> 4 ccgttaccaac acttcaccag gagctgatga ctttcgccga ggaatccacc t 51

```
<210> 5
<211> 34
<212> DNA
<213> Artificial Sequence
```

<220>
<223> Description of Artificial Sequence:Fucus
peroxidase ligation independent cloning (LIC) 5'
primer for full length construct

<400> 5 gacgacgaca atatgctttg ccatgcagcg gaca 34

```
<210> 6
<211> 35
<212> DNA
<213> Artificial Sequence
```

<220>
<223> Description of Artificial Sequence:Fucus
peroxidase ligation independent cloning (LIC) 5'
primer for mid length construct

<pre> <400> 6 gacgacgaca agatggcgcc gaatagaagg gacaa </pre> <pre> <210> 7 <211> 33 <212> DNA <213> Artificial Sequence </pre> <pre> <220> <223> Description of Artificial Sequence:Fucus peroxidase ligation independent cloning (LIC) 5' primer for short construct </pre> <pre> <400> 7 gacgacgaca agatgctctt ccgagcgacc ttc </pre> <pre> <210> 8 <211> 33 <212> DNA <213> Artificial Sequence </pre> <pre> <220> <223> Description of Artificial Sequence:Fucus peroxidase ligation independent cloning (LIC) 3' primer for full length, mid length and short constructs </pre> <pre> <400> 8 gaggagaagc ccgggttgcac taaggctggc agt </pre> <pre> <210> 9 <211> 22 <212> PRT <213> Artificial Sequence </pre> <pre> <220> <223> Description of Artificial Sequence:conserved Fucus vanadium-binding region 1, amino acids 452-473, 1st conserved motif </pre> <pre> <400> 9 Ala Gln Arg Ala Ser Cys Tyr Gln Lys Trp Gln Val His Arg Phe Ala 1 5 10 15 Arg Pro Glu Ala Leu Gly 20 </pre> <pre> <210> 10 <211> 19 <212> PRT <213> Artificial Sequence </pre> <pre> <220> <223> Description of Artificial Sequence:conserved Fucus vanadium-binding region 2, amino acids 528-546, 2nd conserved motif </pre>	35
---	----

```

<400> 10
Pro Thr His Pro Ser Tyr Pro Ser Gly His Ala Thr Gln Asn Gly Ala
1 5 10 15

Phe Ala Thr

<210> 11
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:conserved Fucus
      vanadium-binding region 3, amino acids 591-609,
      3rd conserved motif

<400> 11
Asn Lys Leu Ala Val Asn Val Ala Phe Gly Arg Gln Met Leu Gly Ile
1 5 10 15

His Tyr Arg Phe Asp
20

<210> 12
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:1st conserved
      motif from algal haloperoxidases

<220>
<221> MOD_RES
<222> (1)..(22)
<223> Xaa = any amino acid

<400> 12
Ala Xaa Xaa Xaa Xaa Xaa Tyr Gln Lys Xaa Xaa Xaa His Arg Xaa Xaa
1 5 10 15

Arg Pro Glu Ala Xaa Gly
20

<210> 13
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:1st conserved
      motif from algal and fungal haloperoxidases

<220>
<221> MOD_RES
<222> (2)..(11)
<223> Xaa = any amino acid

```

```

<220>
<221> MOD_RES
<222> (12)
<223> Xaa = any amino acid, present in algal enzymes only

<220>
<221> MOD_RES
<222> (13)..(19)
<223> Xaa = any amino acid

<220>
<221> MOD_RES
<222> (20)
<223> Xaa = any amino acid, present in algal enzymes only

<400> 13
Ala Xaa Xaa Xaa Xaa Xaa Xaa Lys Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10 15

Arg Pro Xaa Xaa Xaa Gly
20

<210> 14
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:2nd conserved
      motif from algal haloperoxidases

<220>
<221> MOD_RES
<222> (1)..(16)
<223> Xaa = any amino acid

<400> 14
Pro Xaa His Pro Ser Tyr Xaa Ser Gly His Ala Xaa Xaa Xaa Gly Ala
1 5 10 15

<210> 15
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:2nd conserved
      motif from algal and fungal haloperoxidases

<220>
<221> MOD_RES
<222> (1)..(16)
<223> Xaa = any amino acid

<400> 15
Pro Xaa Xaa Pro Xaa Tyr Xaa Ser Gly His Ala Xaa Xaa Xaa Gly Ala
1 5 10 15

```

<210> 16
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:2nd conserved
 motif from algal and fungal haloperoxidases,
 phosphatases and other proteins

<220>
 <221> MOD_RES
 <222> (1)
 <223> Ser conserved in some proteins

<220>
 <221> MOD_RES
 <222> (2)
 <223> Tyr conserved in some proteins

<400> 16
 Ser Tyr Pro Ser Gly His
 1 5

<210> 17
 <211> 21
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:3rd conserved
 motif from algal haloperoxidases

<220>
 <221> MOD_RES
 <222> (1)..(21)
 <223> Xaa = any amino acid

<400> 17
 Asn Lys Leu Ala Xaa Asn Xaa Ala Xaa Gly Arg Xaa Met Xaa Gly Xaa
 1 5 10 15

His Tyr Xaa Xaa Asp
 20

<210> 18
 <211> 14
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:3rd conserved
 motif from algal and fungal haloperoxidases

<220>
 <221> MOD_RES
 <222> (1)..(14)
 <223> Xaa = any amino acid

<400> 18
Ala Xaa Xaa Arg Xaa Xaa Xaa Gly Xaa His Xaa Xaa Xaa Asp
1 5 10

<210> 19
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:3rd conserved
motif from algal and fungal haloperoxidases,
phosphatases and other proteins

<220>
<221> MOD_RES
<222> (2)..(9)
<223> Xaa = any amino acid

<220>
<221> MOD_RES
<222> (4)
<223> Gly conserved in some proteins

<220>
<221> MOD_RES
<222> (10)
<223> Asp conserved in some proteins

<400> 19
Arg Xaa Xaa Gly Xaa His Xaa Xaa Xaa Asp
1 5 10

<210> 20
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:6xHis
purification tag

<400> 20
His His His His His His
1 5